

FIGURE 1A

1 CCCC GCGTCGGTCTTCCACCTCACCTTTTCGAGCTGGCCGCGCTTGCTGTGCGCAGTTTC 60
61 GGGG GACTGGACCTTCCCTGGCTTTTAGCAGCGCCGAGCGCCATGGCGACCCTTTGCTGG 120
121 GCAGGTGACCGATTCCGGGTGCCCCAAGGAGCTGGCGTGGGTCTGCCCTGCAGCCGCCCG 180
181 CCTGGACAGGATGTTTGCTAGAGGGCTGAAGAGGAAATATGGTGACCAGGAAGAAGGAGT 240
1 M F A R G L K R K Y G D Q E E G V 17
241 AGAGGGTTTTGGCACTGTCCCTTCCCTATAGCCTGCAGCGACAGTCACTCCTGGACATGTC 300
E G F G T V P S Y S L Q R Q S L L D M S 37
301 CCTTGTCAAGCTCCAGCTCTGTACATGCTAGTGAGCCCAATCTCTGCCGCTCGGTCTCT 360
L V K L Q L C H M L V E P N L C R S V L 57
361 CATCGCCAACACAGTCCGGCAGATCCAGGAGGAAATGAGCCAGGATGGTGTGTGGCATGG 420
I A N T V R Q I Q E E M S Q D G V W H G 77
421 GATGGCACCCAGAAATGTAGATCGGGCACCAGTTGAACGCCTGGTGTCCACAGAGATCCT 480
M A P Q N V D R A P V E R L V S T E I L 97
481 GTGTCTGACAGTGAGGGGAGCTGAGGAAGAGCACCTGCTCCTGAACTGGAAGATGCTCC 540
C R T V R G A E E E H P A P E L E D A P 117
541 CTTGCAAAACTCGGTTTCCGAGCTCCCCATCGTTGGCTCAGCACCAGGGCAAAGGAACCC 600
L Q N S V S E L P I V G S A P G Q R N P 137
601 TCAGAGCAGCCTCTGGGAGATGGACAGCCCAAGAAAACAGGGGAAGCTTTCAGAAGTC 660
Q S S L W E M D S P Q E N R G S F Q K S 157
661 ACTGGACCAGATATTTGAGACCCTGGAGAACAAAACCTCCAGTTCACTGGAGGAACCTCTT 720
L D Q I F E T L E N K N S S S V E E L F 177
721 CTCAGATGTGGACAGCTCCTACTATGACCTGGACACAGTGCTAACAGGAATGATGAGTGG 780
S D V D S S Y Y D L D T V L T G M M S G 197
781 GACCAAGTCCAGTCTCTGCAATGGCCTTGAGGGCTTTGCTGCAGCCACCCCTCCTCCAG 840
T K S S L C N G L E G F A A A T P P P S 217
841 TTCCACTTGCAAGTCTGACCTGGCTGAGCTGGACCATGTGGTAGAGATTCTGGTGGAGAC 900
S T C K S D L A E L D H V V E I L V E T 237
901 CTGAGAGGCCACCCAGTGGGCTAAGGGTGAGGCCACCACTCCCCATGGAGCTCACGTGT 960
*
961 GTTGTGACCCAGAGACAGATAAGCACTTGTCTTAAGAGGGGCTCTGGCTCTTGAGCTCAT 1020
1021 TATCCTTTTGTGTGACATTGGACTCACTGTGGAGGATGGTGTGTACAGCTATGTCTAGT 1080
1081 CTATTTTCAATTAGATAGGTGAACCTTTCTAAAATTAAGTTTTATATGTTTTTGGGCAATA 1140
1141 TTTTGTCTTAAGATATATTTTTTAACTTTTTTATACCTTTAGATTTTTTTTCAGCTATTTTC 1200
1201 TTAAAAGTATATTTTTTCTACAAACATCCTCTGCTGCTACATTAGAAACATTTATAACCT 1260
1261 AAATACGATTGGTGTGTCTATTTTAAAGTTTAAATAGAAAACCTCTTTTGTACTGAGTC 1320
1321 TCTACACTCCCAAGGCAACTGTAAATGTAGCCGGCCGGGTGTTTACATGAGAGGCTCCAG 1380
1381 TATGGTCTACATTCTAGTAGAGCTTGAAAAGAACCATGCACAGCTCCACTGCCCCCTCAC 1440
1441 TGGGTCTGCTCTGGCGGATCGGAGCTCTTCTCTAGCCCCGTGTGCAGGATGGCTTTATT 1500
1501 TATGCCTATTTATATGTAAATGCCACTGAAAGCTAAGGTCTTACTCCTGGAAATCCCAAC 1560
1561 ACCAGTTCTTCAGGGACTGCTGTGAGGCAGTGCCTTATGCAGGTCTTGTCTTGGCCATC 1620
1621 ACTGTCTGGTTCAGGCCAGCACATGTGACATGAGGACATGACATGCCCGAACCACCCA 1680
1681 GCACCACATGCTCCATGTCAAGTGTGTACGTGGAGACCCTGGCTCCCAGGCCTGTGCTC 1740
1741 AGAGAGGGTGTGCAGTCTACGTGTGCTGGGGGGGACGACGGTGACCTGTGCTTGCTTGC 1800
1801 TTTTAAAATGGTGTCTGGACGTTTAAAGTTTAAAACAATCCGACTCCATATGATTTAGG 1860
1861 GTCCTCCACCCTGGGGTGGCCCCTATGCTGTCTGCTTGGATCTCAAAGTCTTGGTACTC 1920
1921 GGCAGTGTGAGACTCCACCCCATGTATCCTTTTTGTTTCTTGTGCTTTTTTTGGACTT 1980
1981 CCCAACCTGAGCCTAAGTTTTATTTTATATGTGCTTCAATATCAACAATGTAAACCTCA 2040
2041 CTTTATTAAAGTATCCAGCAAATGGAAAAAAAAAAAAAAAAA

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FIGURE 1B

1 GGGAAAGCTGGCGGCACAGCCGTGGCGCCTGGCTGAGCAGAGGACCCGGCGGGCGGCCTCG 60
61 CGGGTCAGGACACAATGTTTGCACGAGGACTGAAGAGGAAATGTGTTGGCCACGAGGAAG 120
1 M F A R G L K R K C V G H E E D 16
121 ACGTGGAGGGAGCCCTGGCCGGCTTGAAGACAGTGTCTCATACAGCCTGCAGCGGCAGT 180
V E G A L A G L K T V S S Y S L Q R Q S 36
181 CGCTCCTGGACATGTCTCTGGTGAAGTTGCAGCTTTGCCACATGCTTGTGGAGCCCCAACC 240
L L D M S L V K L Q L C H M L V E P N L 56
241 TGTGCCGCTCAGTCCTCATTCGCAACACGGTCCGGCAGATCCAAGAGGAGATGACGCAGG 300
C R S V L I A N T V R Q I Q E E M T Q D 76
301 ATGGACGTGGCGCAGTGGCACCCTAGGCTGCAGAGCGGGCGCCGCTCGACCGCTTGG 360
G T W R T V A P Q A A E R A P L D R L V 96
361 TCTCCACGGAGATCCTGTGCCGTGCAGCGTGGGGGCAAGAGGGGGCACATCCTGTCTCTG 420
S T E I L C R A A W G Q E G A H P A P G 116
421 GCTTGGGGGACGGCCACACAGGGTCCAGTTTCTGACCTTTGCCCAGTCACCTCAGCAC 480
L G D G H T Q G P V S D L C P V T S A Q 136
481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATGGCCCTCGAGAAAACAGAG 540
A P R H L Q S S A W E M D G P R E N R G 156
541 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACTAAAAACCCAGCT 600
S F H K S L D Q I F E T L E T K N P S C 176
601 GCATGGAAGAGCTGTTCTCAGACGTGGACAGCCCTACTACGACCTGGACACAGTACTGA 660
M E E L F S D V D S P Y Y D L D T V L T 196
661 CAGGCATGATGGGGGGTGCCAGGCCGGGCCCTGCGAAGGGCTCGAGGGCTTGGCTCCGG 720
G M M G G A R P G P C E G L E G L A P A 216
721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCTGGACCACGTGGTGG 780
T P G P S S S C K S D L G E L D H V V E 236
781 AGATCCTGGTGGAGACCTGAGCAGGAGCCCTGAGTGTCTACAGCCGCCCTCTGACGCATTG 840
I L V E T * 241
841 ACACGTGAGCACTGGCTCCCACGGAGGGTGCGCCTGCCGCCAGCGGCCAGCCTTGCTGC 900
901 CCTGTCTGCTGATTCTGAGAAATCCAGAACAGCCATTACCAGTGGGGCTGCAGCCCTA 960
961 GGCCGCTCCCACTCACCTCCCCCTGTGGAGCGCCAGGCAGAGGCTGTTCTGGAAGGCTT 1020
1021 TTTGTCTTCTGACGTCCCCACAGCCCTGGGCCCCCTCGTGTCTCTTTGTGTCCCCACTGT 1080
1081 AGAGGACGGTGAGCCGCAGCTGCATCAACCTCCTTTTACCTTTAGATAGGTGAATTTTTTA 1140
1141 CAATTCAGTTTTACATGTTTTTGGGCAGTATTTTGTCTTAAGATATATTTTTTAACTTTT 1200
1201 TATACCTTATCTCTTTAGATTTTTTTCAGCTATTTTCTTAAAAGTATATTTTTTCTATAAA 1260
1261 CATCCTTTGCTGCTACATTAGAACTTTTATAGCCTAAACAATTGCAGTTGGTGTGTTTCA 1320
1321 TTTTTTTAAGGTTTAAATAAGGGTTTTTGTGTTTTGTTTTGTTTTTGCAGTGAGCATCAC 1380
1381 TACAGTCTCAGTCAACAGTGTGAATGTATCATGTTTTACTTTAAATGTGTGTGTGATACT 1440
1441 TCTTCATTATGTCTGCGCTGCAGTGAGACCTGGGTGAAAATCAGGAGCCGCACACAGCC 1500
1501 ACATCTTCTTAGACCTAAGAGTAAATTATGGAGGATTTTATTTATGTCTATTTATATGTA 1560
1561 AATGTCAATTGAAGACAAAGGTCAAATATTTGTCTGTTTGTAGATCACAGGCACCAAGTTGG 1620
1621 TCTTCAGGGACCTCATAGCCCCCTCGGTGGTGCCTTCTCAAGGCAGTGTTCCTGGAGGCTC 1680
1681 CCATCAGGGTCAGCCCATGCACCTGCCCTGGGTGAGGAAGTAGCATTGCTGCTGGATGAG 1740
1741 AAACGCCCTGCGTGCTCTGTTAGACTGGTGTGAAACAAAAGGTTAAGGCTAGGTTGAAG 1800
1801 TCTAGAATGAAAGAAATCTGAATCCATGTCAATCATAACCCCTTGATCTGTAGTGTGATG 1860
1861 GGTGCTGCCGCAGGCAGGGAGTGAGCTGGGGGTGCCTGCAGCCTTCCACTCCTGCCCCGC 1920
1921 CTCACCCACATGCTCCCTGTTTCTCATGCTTTCTCTAACTTCCTCACCCTTAACCCAA 1980
1981 AAGGTGTGTTTTCTTTTGTGCATATAGCCATTCTTAAATATCAGTGATGTAAACCTCACT 2040
2041 TTATTAATAAATTATCCAGCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 2

Mouse Hepp	1	MFARGLKRRKYG---DOEEGVGFGTVPSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRSV
Human HEPP	1	MFARGLKRRKCVGHEDVEGALAGLKTVSSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRSV
Mouse Hepp	57	LIANTVRQIQEEMSQDGVVHGMAPONVDRAPVERLVSTEILCRTVRCAGEEHPAPELEDA
Human HEPP	61	LIANTVRQIQEEMTQDGTWRITVAPOAAERAPLDRLVSTEILCRAAWGQEGAHAPAGLGCG
Mouse Hepp	117	PLONSVSELPVGSAPGORNPOSSLWEMDSPQENRGSEFKSLDQIFETLEKNKSSVEEL
Human HEPP	121	HTQGPVSDLCPVTSQAQPRHLOSSAWEMDGPENRGSEFKSLDQIFETLETKNPSCMEEL
Mouse Hepp	177	FSDVDSSTYDLDTVLTGMMSCGRSSLCNGLEGFAAATPPSSSTCKSDLAELDHVVEILVE
Human HEPP	181	FSDVDSPTYDLDTVLTGMMGCARPGPCEGLEGLAPATPGPSSSCKSDLAELDHVVEILVE
Mouse Hepp	237	T
Human HEPP	241	T

FIGURE 3

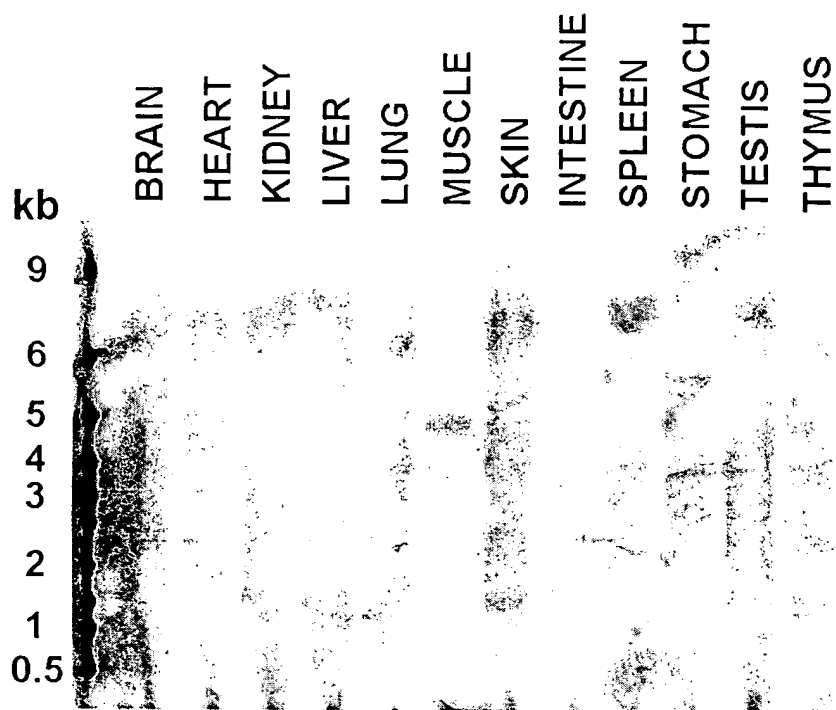
Zebrafish Hepp	1	MFSGTKRRKFADGGEETISDDGLVAARVASSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRS
Mouse Hepp	1	MFARGLKRRKYG---DOEEGVGFGTVPSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRS
Human HEPP	1	MFARGLKRRKCVGH-EDVEGALAGLKTVSSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRS
Zebrafish Hepp	61	VLIANTVRQIQEEMTHDGSWHMVTFAFCGASQSPSERLVATEMLCR-----
Mouse Hepp	56	VLIANTVRQIQEEMSQDGVVHGMAPONVDR--APVERLVSTEILCRTVRCAGEEHPAPEL
Human HEPP	60	VLIANTVRQIQEEMTQDGTWRITVAPOAAER--APLDRLVSTEILCRAAWGQEGAHAPAGL

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FIGURE 4A



FIGURE 4B



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FIGURE 5

New U.S. Patent Application
 Inventor: R. JURECIC *et al.*
 Title: P, A Novel Gene with a Role in
 Hematopoietic and Neural Development"
 Attorney Docket No. 39532.176599
 Sheet 5 of 14

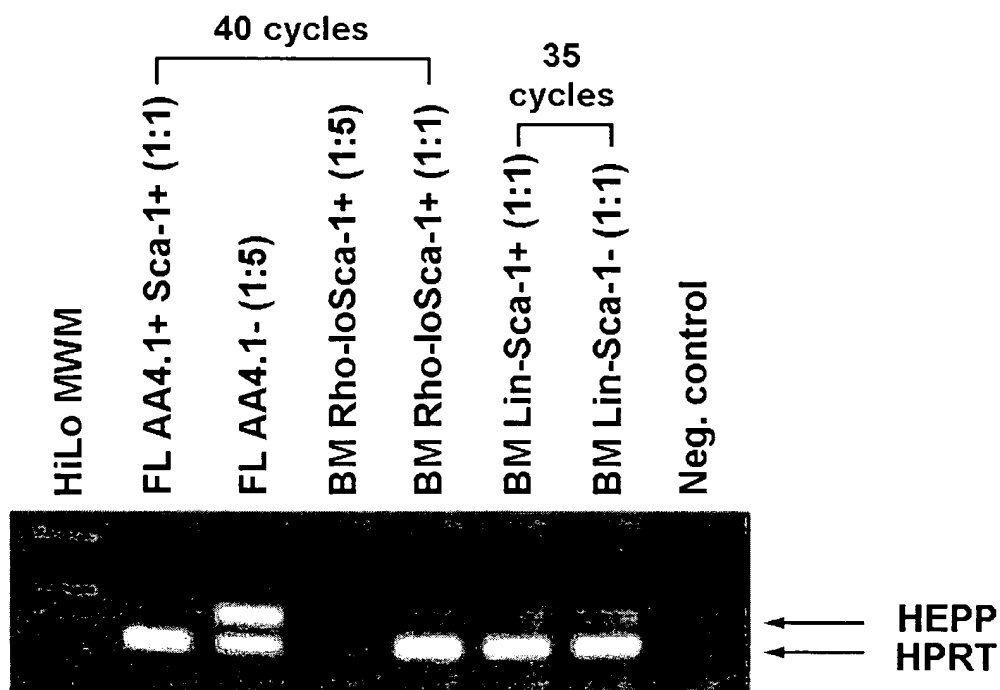


FIGURE 6

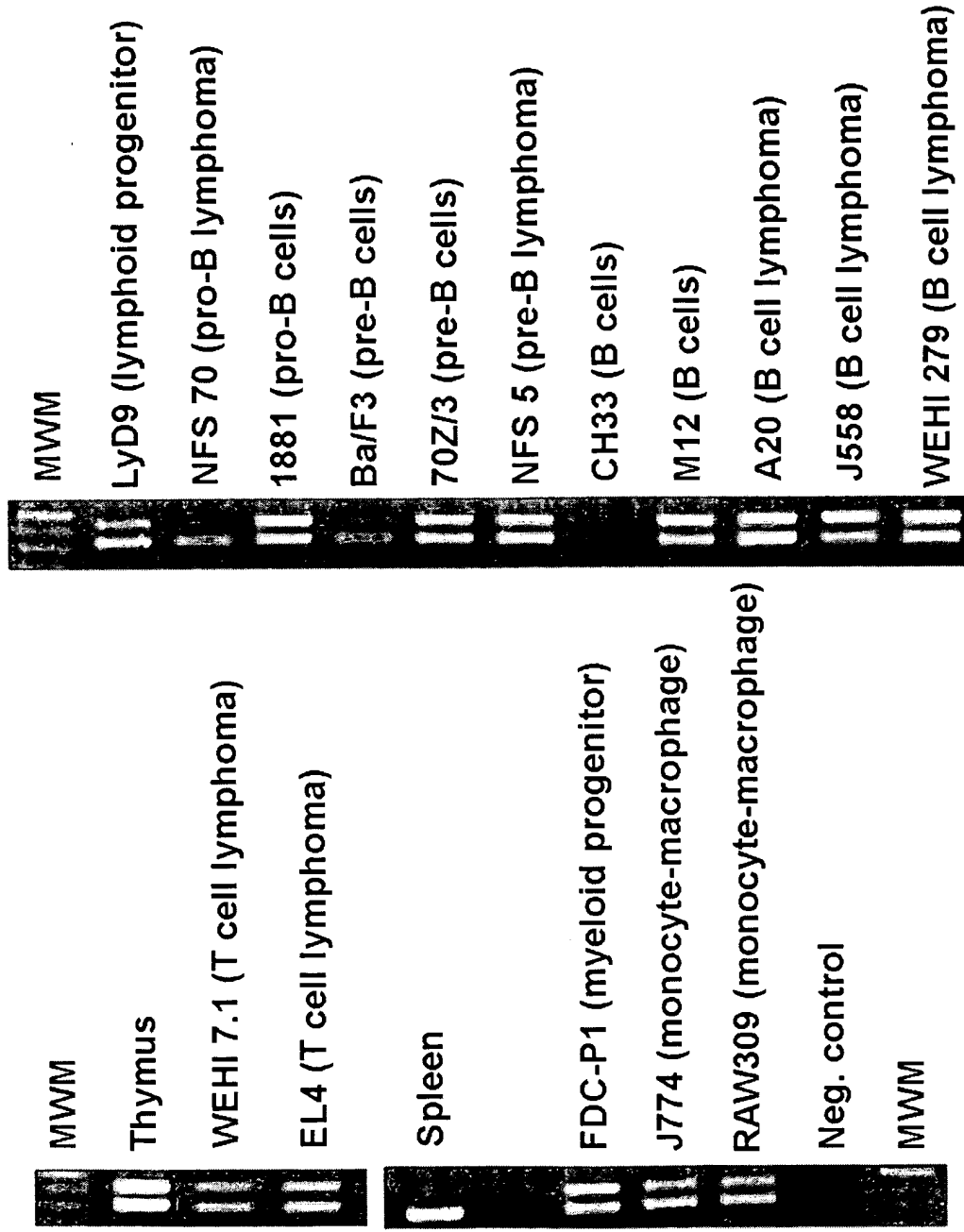
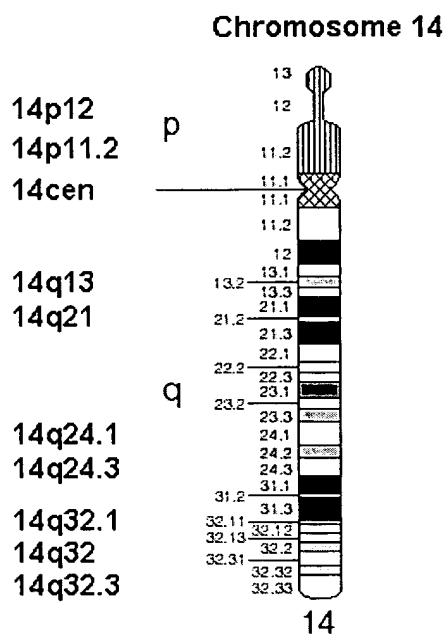


FIGURE 7



translocation breakpoints

FIGURE 8

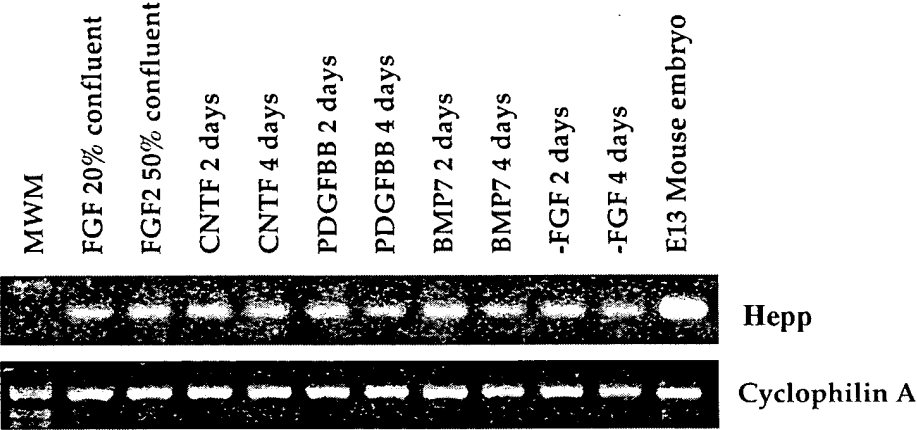


FIGURE 9

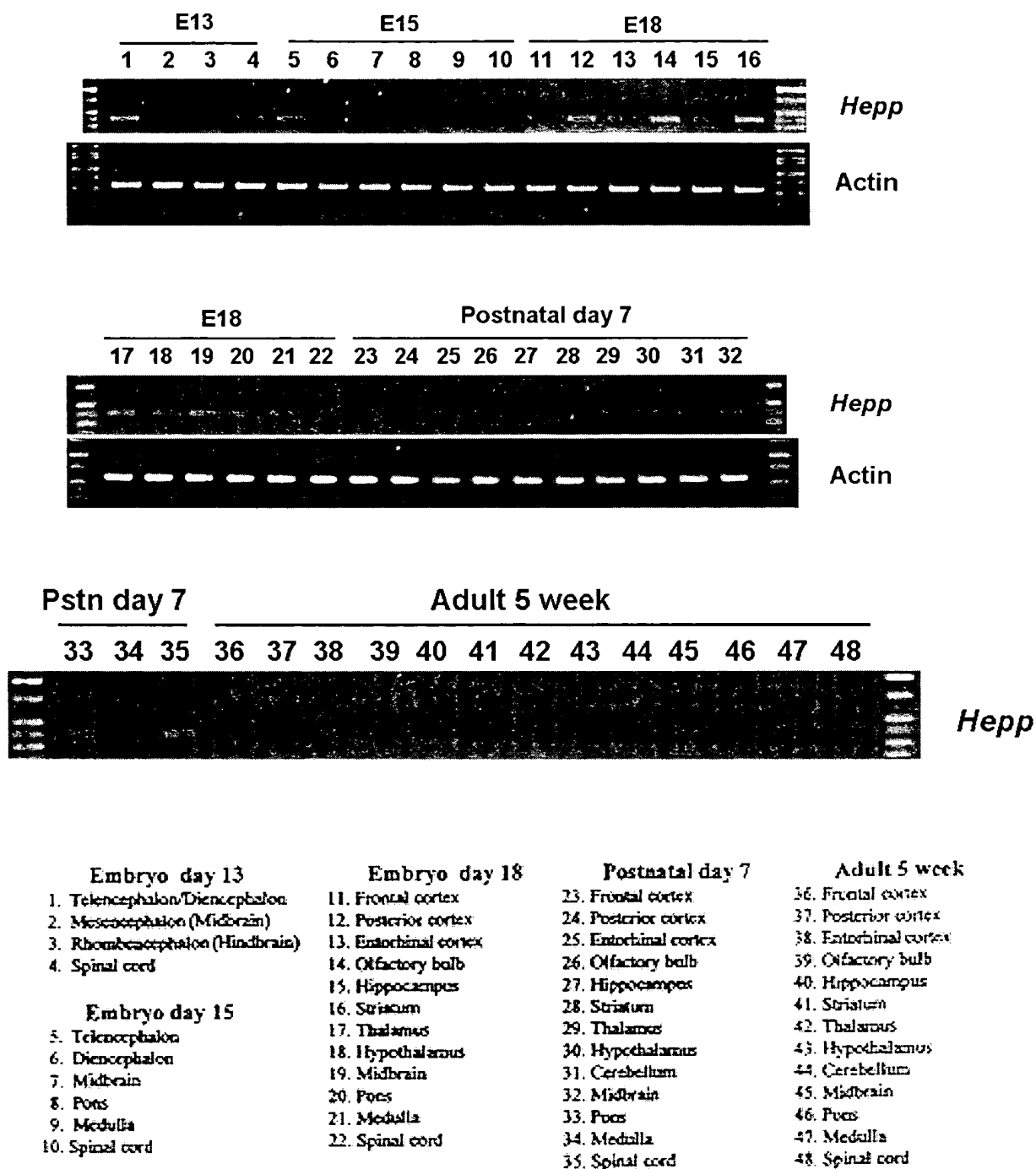


FIGURE 10

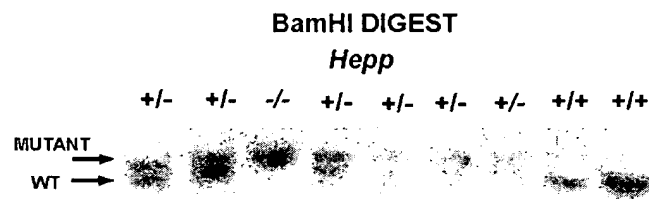
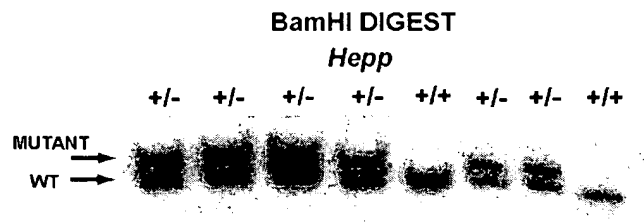


FIGURE 11

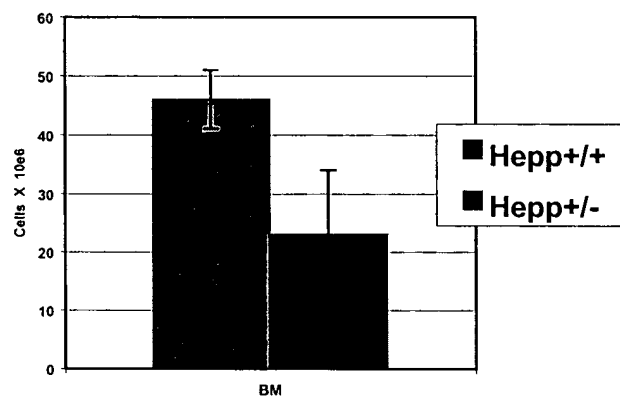


FIGURE 12

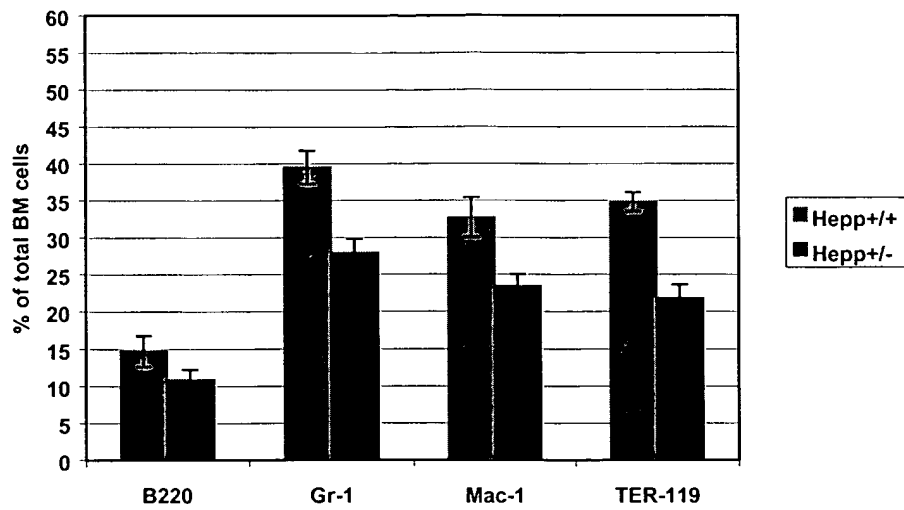


FIGURE 13

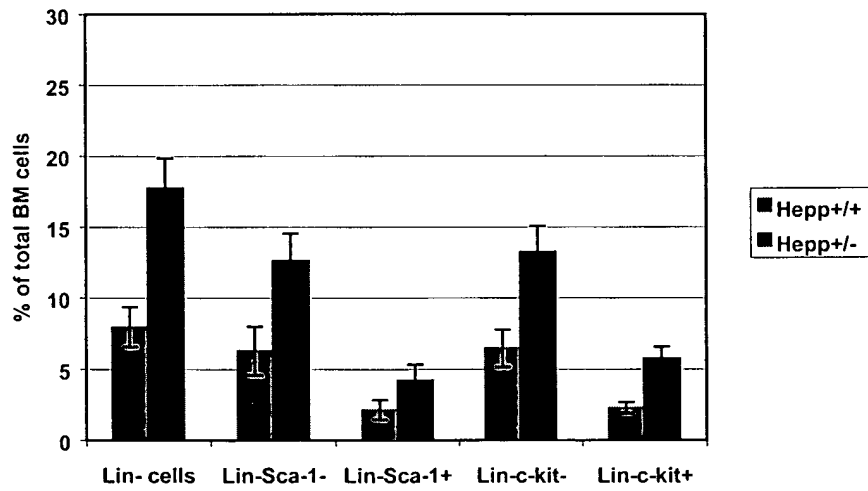


FIGURE 14

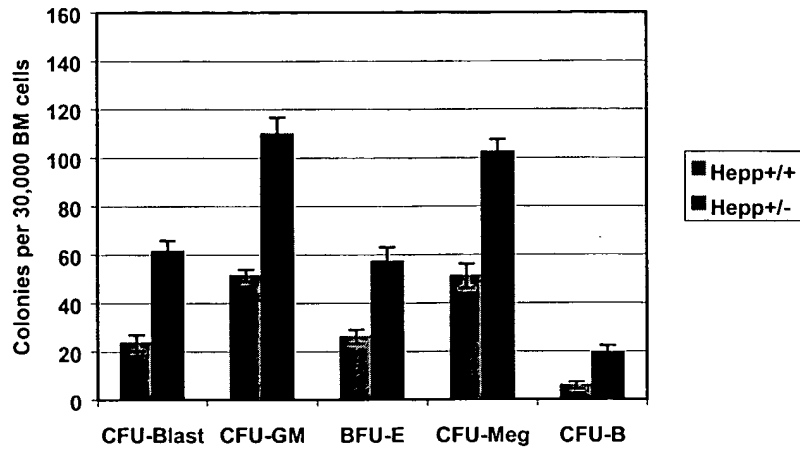


FIGURE 15A-B

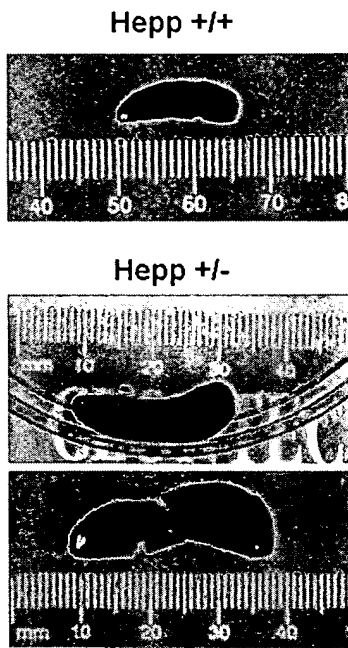


FIGURE 15C

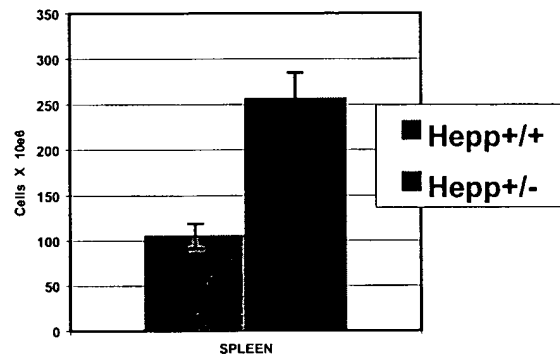


FIGURE 16

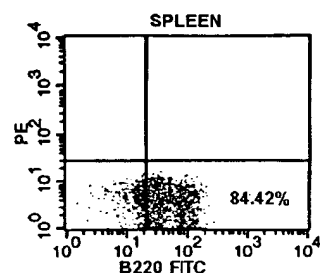
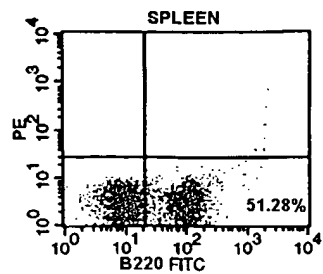
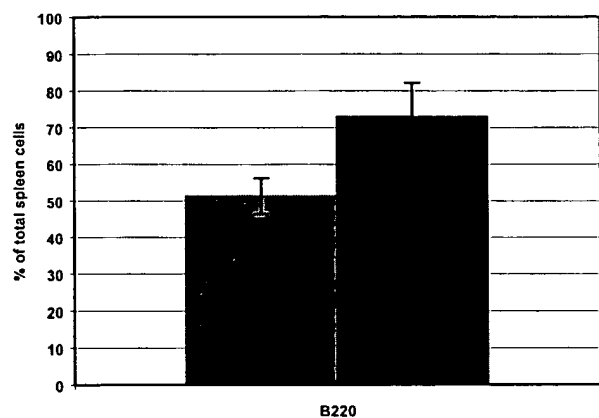


FIGURE 17

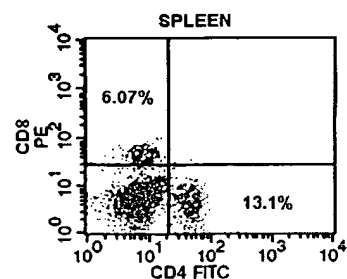
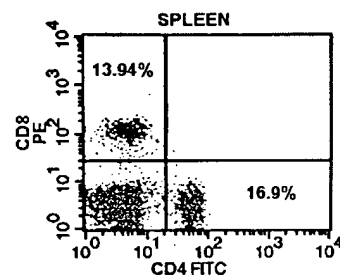
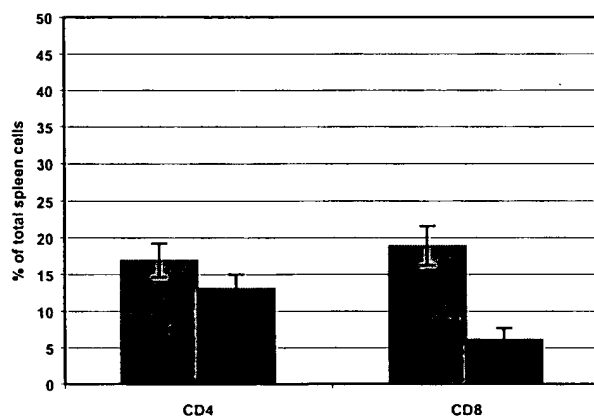


FIGURE 18A



FIGURE 18B



FIGURE 18C



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